

SEQUENCE LISTING

78-0B10 amino acid sequence (SEQ ID NO:1)

5	Met Ala Asp Lys Asn Ile Leu Tyr Gly Pro Glu Pro Phe Tyr Pro Leu	1	5	10	15
	Ala Asp Gly Thr Ala Gly Glu Gln Met Phe Asp Ala Leu Ser Arg Tyr	20	25	30	
	Ala Asp Ile Ser Gly Cys Ile Ala Leu Thr Asn Ala His Thr Lys Glu	35	40	45	
10	Asn Val Leu Tyr Glu Glu Phe Leu Lys Leu Ser Cys Arg Leu Ala Glu	50	55	60	
	Ser Phe Lys Lys Tyr Gly Leu Lys Gln Asn Asp Thr Ile Ala Val Cys	65	70	75	80
	Ser Glu Asn Gly Leu Gln Phe Phe Leu Pro Val Ile Ala Ser Leu Tyr	85	90	95	
15	Leu Gly Ile Ile Ala Ala Pro Val Ser Asp Lys Tyr Ile Glu Arg Glu	100	105	110	
	Leu Ile His Ser Leu Gly Ile Val Lys Pro Arg Ile Ile Phe Cys Ser	115	120	125	
20	Lys Asn Thr Phe Gln Lys Val Leu Asn Val Lys Ser Lys Leu Lys Ser	130	135	140	
	Val Glu Thr Ile Ile Ile Leu Asp Leu Asn Glu Asp Leu Gly Gly Tyr	145	150	155	160
	Gln Cys Leu Asn Asn Phe Ile Ser Gln Asn Ser Asp Ser Asn Leu Asp	165	170	175	
25	Val Lys Lys Phe Lys Pro Tyr Ser Phe Asn Arg Asp Asp Gln Val Ala	180	185	190	
	Leu Val Met Phe Ser Ser Gly Thr Thr Gly Val Pro Lys Gly Val Met	195	200	205	
30	Leu Thr His Lys Asn Ile Val Ala Arg Phe Ser Leu Ala Lys Asp Pro	210	215	220	
	Thr Phe Gly Asn Ala Ile Asn Pro Thr Thr Ala Ile Leu Thr Val Ile	225	230	235	240
	Pro Phe His His Gly Phe Gly Met Met Thr Thr Leu Gly Tyr Phe Thr	245	250	255	
35	Cys Gly Phe Arg Val Val Leu Met His Thr Phe Glu Glu Lys Leu Phe	260	265	270	
	Leu Gln Ser Leu Gln Asp Tyr Lys Val Glu Ser Thr Leu Leu Val Pro	275	280	285	
40	Thr Leu Met Ala Phe Leu Ala Lys Ser Ala Leu Val Glu Lys Tyr Asp	290	295	300	
	Leu Ser His Leu Lys Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys	305	310	315	320
	Glu Ile Gly Glu Met Val Lys Lys Arg Phe Lys Leu Asn Phe Val Arg	325	330	335	
45					

Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Val Leu Ile Thr Pro
 340 345 350
 Lys Gly Asp Ala Arg Pro Gly Ser Thr Gly Lys Ile Val Pro Phe His
 355 360 365
 5 Ala Val Lys Val Val Asp Pro Thr Thr Gly Lys Ile Leu Gly Pro Asn
 370 375 380
 Glu Pro Gly Glu Leu Tyr Phe Lys Gly Ala Met Ile Met Lys Gly Tyr
 385 390 395 400
 Tyr Asn Asn Glu Glu Ala Thr Lys Ala Ile Ile Asp Asn Asp Gly Trp
 10 405 410 415
 Leu Arg Ser Gly Asp Ile Ala Tyr Tyr Asp Asn Asp Gly His Phe Tyr
 420 425 430
 Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln Val
 435 440 445
 15 Ala Pro Ala Glu Ile Glu Gly Ile Leu Leu Gln His Pro Tyr Ile Val
 450 455 460
 Asp Ala Gly Val Thr Gly Ile Pro Asp Glu Ala Ala Gly Glu Leu Pro
 465 470 475 480
 Ala Ala Gly Val Val Val Gln Thr Gly Lys Tyr Leu Asn Glu Gln Ile
 20 485 490 495
 Val Gln Asp Phe Val Ser Ser Gln Val Ser Thr Ala Lys Trp Leu Arg
 500 505 510
 Gly Gly Val Lys Phe Leu Asp Glu Ile Pro Lys Gly Ser Thr Gly Lys
 515 520 525
 25 Ile Asp Arg Lys Val Leu Arg Gln Met Phe Glu Lys His Thr Asn Gly
 530 535 540

90-1B5 amino acid sequence (SEQ ID NO:2)

30 Met Ala Asp Lys Asn Ile Leu Tyr Gly Pro Glu Pro Phe Tyr Pro Leu
 1 5 10 15
 Glu Asp Gly Thr Ala Gly Glu Gln Met Phe Asp Ala Leu Ser Arg Tyr
 20 25 30
 35 Ala Asp Ile Pro Gly Cys Ile Ala Leu Thr Asn Ala His Thr Lys Glu
 35 40 45
 Asn Val Leu Tyr Glu Glu Phe Leu Lys Leu Ser Cys Arg Leu Ala Glu
 50 55 60
 Ser Phe Lys Lys Tyr Gly Leu Lys Gln Asn Asp Thr Ile Ala Val Cys
 40 65 70 75 80
 Ser Glu Asn Gly Leu Gln Phe Phe Leu Pro Val Ile Ala Ser Leu Tyr
 85 90 95
 Leu Gly Ile Ile Val Ala Pro Val Asn Asp Lys Tyr Ile Glu Arg Glu
 100 105 110
 45 Leu Ile His Ser Leu Gly Ile Val Lys Pro Arg Ile Val Phe Cys Ser
 115 120 125
 Lys Asn Thr Phe Gln Lys Val Leu Asn Val Lys Ser Lys Leu Lys Ser

	130	135	140	
	Ile	Glu	Thr	Ile
	145	150	155	160
	Gln	Cys	Leu	Asn
5	165	170	175	
	Val	Lys	Lys	Phe
	180	185	190	
	Leu	Ile	Met	Phe
10	195	200	205	
	Leu	Thr	His	Lys
	210	215	220	
	Thr	Phe	Gly	Asn
	225	230	235	240
	Pro	Phe	His	His
15	245	250	255	
	Cys	Gly	Phe	Arg
	260	265	270	
	Leu	Gln	Ser	Leu
20	275	280	285	
	Thr	Leu	Met	Ala
	290	295	300	
	Leu	Ser	His	Leu
	305	310	315	320
	Glu	Ile	Gly	Glu
25	325	330	335	
	Gln	Gly	Tyr	Gly
	340	345	350	
	Lys	Gly	Asp	Ala
30	355	360	365	
	Ala	Val	Lys	Val
	370	375	380	
	Glu	Pro	Gly	Glu
	385	390	395	400
	Tyr	Asn	Asn	Glu
35	405	410	415	
	Leu	Arg	Ser	Gly
	420	425	430	
	Ile	Val	Asp	Arg
40	435	440	445	
	Ala	Pro	Ala	Glu
	450	455	460	
	Asp	Ala	Gly	Val
	465	470	475	480
	Ala	Ala	Gly	Val
45	485	490	495	
	Val	Gln	Asp	Tyr
	500	505	510	

Gly Gly Val Lys Phe Leu Asp Glu Ile Pro Lys Gly Ser Thr Gly Lys
515 520 525
Ile Asp Arg Lys Val Leu Arg Gln Met Phe Glu Lys His Thr Asn Gly
530 535 540

5

133-1B2 amino acid sequence (SEQ ID NO:3)

Met Ala Asp Lys Asn Ile Leu Tyr Gly Pro Glu Pro Phe Tyr Pro Leu
1 5 10 15
10 Glu Asp Gly Thr Ala Gly Glu Gln Met Phe Asp Ala Leu Ser Arg Tyr
20 25 30
Ala Asp Ile Pro Gly Cys Ile Ala Leu Thr Asn Ala His Thr Lys Glu
35 40 45
15 Asn Val Leu Tyr Glu Glu Phe Leu Lys Leu Ser Cys Arg Leu Ala Glu
50 55 60
Ser Phe Lys Lys Tyr Gly Leu Lys Gln Asn Asp Thr Ile Ala Val Cys
65 70 75 80
20 Ser Glu Asn Ser Leu Gln Phe Phe Leu Pro Val Ile Ala Ser Leu Tyr
85 90 95
Leu Gly Ile Ile Val Ala Pro Val Asn Asp Lys Tyr Ile Glu Arg Glu
100 105 110
Leu Ile His Ser Leu Gly Ile Val Lys Pro Arg Ile Val Phe Cys Ser
115 120 125
25 Lys Asn Thr Phe Gln Lys Val Leu Asn Val Lys Ser Lys Leu Lys Ser
130 135 140
Ile Glu Thr Ile Ile Ile Leu Asp Leu Asn Asp Asp Leu Gly Gly Tyr
145 150 155 160
30 Gln Cys Leu Asn Asn Phe Ile Ser Gln Asn Ser Asp Ser Asn Leu Asp
165 170 175
Val Lys Lys Phe Lys Pro Tyr Ser Phe Asn Arg Asp Asp Gln Val Ala
180 185 190
Leu Ile Met Phe Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met
195 200 205
35 Leu Thr His Lys Asn Ile Val Ala Arg Phe Ser Ile Ala Lys Asp Pro
210 215 220
Thr Phe Gly Asn Ala Ile Asn Pro Thr Ser Ala Ile Leu Thr Val Ile
225 230 235 240
Pro Phe His His Gly Phe Gly Met Met Thr Thr Leu Gly Tyr Phe Thr
245 250 255
40 Cys Gly Phe Arg Val Val Leu Met His Thr Phe Glu Glu Lys Leu Phe
260 265 270
Leu Gln Ser Leu Gln Asp Tyr Lys Val Glu Ser Thr Leu Leu Val Pro
275 280 285
45 Thr Leu Met Ala Phe Leu Ala Lys Ser Ala Leu Val Glu Lys Tyr Asp
290 295 300
Leu Ser His Leu Lys Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys

	Leu Ile His Ser Leu Gly Ile Val Lys Pro Arg Ile Val Phe Cys Ser
	115 120 125
	Lys Asn Thr Phe Gln Lys Val Leu Asn Val Lys Ser Lys Leu Lys Ser
	130 135 140
5	Ile Glu Thr Ile Ile Ile Leu Asp Leu Asn Glu Asp Leu Gly Gly Tyr
	145 150 155 160
	Gln Cys Leu Asn Asn Phe Ile Ser Gln Asn Ser Asp Ser Asn Leu Asp
	165 170 175
	Val Lys Lys Phe Lys Pro Tyr Ser Phe Asn Arg Asp Asp Gln Val Ala
10	180 185 190
	Ser Ile Met Phe Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met
	195 200 205
	Leu Thr His Lys Asn Ile Val Ala Arg Phe Ser Ile Ala Lys Asp Pro
	210 215 220
15	Thr Phe Gly Asn Ala Ile Asn Pro Thr Ser Ala Ile Leu Thr Val Ile
	225 230 235 240
	Pro Phe His His Gly Phe Gly Met Met Thr Thr Leu Gly Tyr Phe Thr
	245 250 255
	Cys Gly Phe Arg Val Val Leu Met His Thr Phe Glu Glu Lys Leu Phe
20	260 265 270
	Leu Gln Ser Leu Gln Asp Tyr Lys Val Glu Ser Thr Leu Leu Val Pro
	275 280 285
	Thr Leu Met Ala Phe Leu Ala Lys Ser Ala Leu Val Glu Lys Tyr Asp
	290 295 300
25	Leu Ser His Leu Lys Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys
	305 310 315 320
	Glu Ile Gly Glu Met Val Lys Lys Arg Phe Lys Leu Asn Phe Val Arg
	325 330 335
	Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Val Leu Ile Thr Pro
30	340 345 350
	Lys Gly Asp Ala Lys Pro Gly Ser Thr Gly Lys Ile Val Pro Leu His
	355 360 365
	Ala Val Lys Val Val Asp Pro Thr Thr Gly Lys Ile Leu Gly Pro Asn
	370 375 380
35	Glu Pro Gly Glu Leu Tyr Phe Lys Gly Pro Met Ile Met Lys Gly Tyr
	385 390 395 400
	Tyr Asn Asn Glu Glu Ala Thr Lys Ala Ile Ile Asp Asn Asp Gly Trp
	405 410 415
	Leu Arg Ser Gly Asp Ile Ala Tyr Tyr Asp Asn Asp Gly His Phe Tyr
40	420 425 430
	Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln Val
	435 440 445
	Ala Pro Ala Glu Ile Glu Gly Ile Leu Leu Gln His Pro Tyr Ile Val
	450 455 460
45	Asp Ala Gly Val Thr Gly Ile Pro Asp Glu Ala Ala Gly Glu Leu Pro
	465 470 475 480
	Ala Ala Gly Val Val Val Gln Thr Gly Lys Tyr Leu Asn Glu Gln Ile

	485	490	495	
	Val Gln Asp Tyr	Val Ala Ser Gln	Val Thr Ala Lys Trp	Leu Arg
	500	505	510	
5	Gly Gly Val Lys Phe	Leu Asp Glu Ile	Pro Lys Gly Ser Thr	Gly Lys
	515	520	525	
	Ile Asp Arg Lys	Val Leu Arg Gln	Met Leu Glu Lys	His Thr Asn Gly
	530	535	540	

78-0B10 (SEQ ID NO:5)

10 GGATCCAATGGCAGATAAGAATATTTTATATGGGCCCCGAACCATTTTATCCCT
 TGGCTGATGGGACGGCTGGAGAACAGATGTTTGACGCATTATCTCGTTATGC
 AGATATTTCCGGATGCATAGCATTGACAAATGCTCATACAAAAGAAAATGTT
 TTATATGAAGAGTTTTTAAAATTGTCGTGTCGTTTAGCGGAAAGTTTTAAAAA
 GTATGGATTAAAACAAAACGACACAATAGCGGTGTGTAGCGAAAATGGTTTG
 15 CAATTTTTCCTTCCTGTAATTGCATCATTGTATCTTGGAATAATTGCAGCACCT
 GTTAGTGATAAATACATTGAACGTGAATTAATACACAGTCTTGGTATTGTAAA
 ACCACGCATAATTTTTTGTCTCCAAGAATACTTTCAAAAAGTACTGAATGTAA
 AATCTAAATTAAAATCTGTAGAACTATTATTATATTAGACTTAAATGAAGAC
 TTAGGAGGTTATCAATGCCTCAACAACCTTTATTTCTCAAAATCCGATAGTAA
 20 TCTGGACGTAAAAAAATTTAAACCATATTCTTTTAATCGAGACGATCAGGTTG
 CGTTGGTAATGTTTTCTTCTGGTACAACCTGGTGTTCGGAAGGGAGTCATGCTA
 ACTCACAAGAATATTGTTGCACGATTTTCTCTTGCAAAAGATCCTACTTTTGG
 TAACGCAATTAATCCACGACAGCAATTTTAACGGTAATACCTTCCACCATG
 GTTTTGGTATGATGACCACATTAGGATACTTTACTTGTGGATTCCGAGTTGTT
 25 CTAATGCACACGTTTGAAGAAAAACTATTTCTACAATCATTACAAGATTATAA
 AGTGGAAAGTACTTTACTTGTACCAACATTAATGGCATTCTTGCAAAAAGTG
 CATTAGTTGAAAAGTACGATTTATCGCACTTAAAAGAAATTGCATCTGGTGG
 CGCACCTTTATCAAAAAGAAATTGGGGAGATGGTGAAAAAACGGTTTAAATTA
 AACTTTGTCAGGCAAGGGTATGGATTAACAGAAACCACTTCGGCTGTTTTAAT
 30 TACACCGAAAGGTGACGCCAGACCGGGATCAACTGGTAAAATAGTACCATT
 CACGCTGTTAAAGTTGTCTGATCCTACAACAGGAAAAATTTGGGGCCAAATG
 AACCTGGAGAATTGTATTTTAAAGGCGCCATGATAATGAAGGGTTATTATAA
 TAATGAAGAAGCTACTAAAGCAATTATTGATAATGACGGATGGTTGCGCTCT
 35 GGTGATATTGCTTATTATGACAATGATGGCCATTTTATATTGTGGACAGGCT
 GAAGTCATTAATTAATATAAAGGTTATCAGGTTGCACCTGCTGAAATTGAG
 GGAATACTCTTACAACATCCGTATATTGTTGATGCCGGCGTTACTGGTATACC
 GGATGAAGCCGCGGGCGAGCTTCCAGCTGCAGGTGTTGTAGTACAGACTGGA
 AAATATCTAAACGAACAAATCGTACAAGATTTTGTTTCCAGTCAAGTTTCAAC
 AGCCAAATGGCTACGTGGTGGGGTGAAATTTTGGATGAAATTCCCAAAGGA
 40 TCAACTGGAAAAATTGACAGAAAAGTGTTAAGACAAATGTTTGAAAAACACA
 CCAATGGG

90-1B5 (SEQ ID NO:6)

45 GGATCCAATGGCAGATAAGAATATTTTATATGGGCCCCGAACCATTTTATCC
 CTTGGAAGA 60
 TGGGACGGCTGGAGAACAGATGTTTGACGCATTATCTCGTTATGCAGATA
 TTCCGGGCTG 120

CATAGCATTGACAAATGCTCATACAAAAGAAAATGTTTTATATGAAGAGT
TTCTGAAACT 180
GTCGTGTCGTTTAGCGGAAAGTTTTAAAAAGTATGGATTAACAAAACG
ACACAATAGC 240
5 GGTGTGTAGCGAAAATGGTCTGCAATTTTTCTTCCTGTAATTGCATCATT
GTATCTTGG 300
AATAATTGTGGCACCTGTTAACGATAAATACATTGAACGTGAATTAATAC
ACAGTCTTGG 360
TATTGTAAAACCGCATAGTTTTTTGCTCCAAGAATACTTTTCAAAAAGT
10 ACTGAATGT 420
AAAATCTAAATTAATACTATTGAACTATTATTATATTAGACTTAAATGA
AGACTTAGG 480
AGGTTATCAATGCCTCAACAACCTTTATTTCTCAAAATTCCGATAGTAATCT
GGACGTAAC 540
15 AAAATTTAAACCATATTCTTTTAATCGAGACGATCAGGTTGCGTTGATTAT
GTTTTCTTC 600
TGGTACAACCTGGTCTGCCGAAGGGAGTCATGCTAACTCACAAGAATATTG
TTGCACGATT 660
TTCTCTTGCAAAAGATCCTACTTTTGGTAACGCAATTAATCCCACGACAGC
20 AATTTTAAC 720
GGTAATACCTTTCCACCATGGTTTTTGGTATGATGACCACATTAGGATACTT
TACTTGTGG 780
ATTCCGAGTTGTTCTAATGCACACGTTTGAAGAAAACTATTTCTACAATC
ATTACAAGA 840
25 TTATAAAGTGGAAGTACTTTACTTGTACCAACATTAATGGCATTCTTGC
AAAAAGTGC 900
ATTAGTTGAAAAGTACGATTTATCGCACTTAAAAGAAATTGCATCTGGTG
GCGCACCTTT 960
ATCAAAAGAAATTGGGGAGATGGTGAAAAAACGGTTTAAATTAACTTTG
30 TCAGGCAAGG 1020
GTATGGATTAACAGAAACCACTTCGGCTGTTTTAATTACACCGAAAGGTG
ACGCCAAACC 1080
GGGATCAACTGGTAAAATAGTACCATTTACGCTGTAAAGTTGTGATCC
TACAACAGG 1140
35 AAAAATTTTGGGGCCAAATGAACCTGGAGAATTGTATTTTAAAGGCCCGA
TGATAATGAA 1200
GGGTTATTATAATAATGAAGAAGCTACTAAAGCAATTATTGATAATGACG
GATGGTTGCG 1260
CTCTGGTGATATTGCTTATTATGACAATGATGGCCATTTTTATATTGTGGA
40 CAGGCTGAA 1320
GTCAGTGAATTAATAAAGGTTATCAGGTTGCACCTGCTGAAATTGAGG
GAATACTCTT 1380
ACAACATCCGTATATTGTTGATGCCGGCGTTACTGGTATACCGGATGAAG
CCGCGGGCGA 1440
45 GCTTCCAGCTGCAGGTGTTGTAGTACAGACTGGAAAATATCTAAACGAAC
AAATCGTACA 1500

AGATTATGTTGCCAGTCAAGTTTCAACAGCCAAATGGCTACGTGGTGGGG
TGAAATTTTT 1560
GGATGAAATTCCCAAAGGATCAACTGGAAAAATTGACAGAAAAGTGTTA
AGACAAATGTT 1620
5 TGAAAAACACACCAATGGG 1639

133-1B2 (SEQ ID NO:7)

AGATCCAATGGCAGATAAGAATATTTTATATGGGCCCCGAACCATTTTATCCCT
TGGAAGATGGGACGGCTGGAGAACAGATGTTTGACGCATTATCTCGTTATGC
10 AGATATTCCGGGCTGCATAGCATTGACAAATGCTCATACAAAAGAAAATGTT
TTATATGAAGAGTTTCTGAAACTGTCGTGTCGTTTAGCGGAAAGTTTTAAAAA
GTATGGATTA AAAACAAAACGACACAATAGCGGTGTGTAGCGAAAATAGTCTG
CAATTTTTCCTTCCTGTAATTGCATCATTGTATCTTGGAATAATTGTGGCACCT
GTTAACGATAAATACATTGAACGTGAATTAATACACAGTCTTGGTATTGTAA
15 AACCACGCATAGTTTTTTGCTCCAAGAATACTTTTCAAAAAGTACTGAATGTA
AAATCTAAATTAAAATCTATTGAACTATTATTATATTAGACTTAAATGATGA
CTTAGGAGGTTATCAATGCCTCAACAACTTTATTTCTCAAAATTCCGATAGTA
ATCTGGACGTAAAAAAATTTAAACCATATTCTTTAATCGAGACGATCAGGTT
GCGTTGATTATGTTTTCTTCTGGTACAACCTGGTCTGCCGAAGGGAGTCATGCT
20 AACTCACAAGAATATTGTTGCACGATTTTCTATTGCAAAAGATCCTACTTTTG
GTAACGCAATTAATCCCACGTCAGCAATTTTAACGGTAATACCTTTCCACCAT
GGTTTTGGTATGATGACCACATTAGGATACTTTACTTGTGGATTCCGAGTTGT
TCTAATGCACACGTTTGAAGAAAAACTATTTCTACAATCATTACAAGATTATA
AAGTGGAAGTACTTTACTTGTACCAACATTAATGGCATTTCCTTGCAAAAAGT
25 GCATTAGTTGAAAAGTACGATTTATCGCACTTAAAAGAAATTGCATCTGGTG
GCGCACCTTTATCAAAAGAAATTGGGGAGATGGTGAAAAAACGGTTTAAATT
AAACTTTGTCAGGCAAGGGTATGGATTAACAGAAACCACTTCGGCTGTTTTA
ATTACACCGAAAGGTGACGCCAAACCGGGATCAACTGGTAAAATAGTACCAT
TTCACGCTGTAAAGTTGTGCGATCCTACAACAGGAAAAATTTTGGGGCCAAA
30 TGAACCTGGAGAATTGTATTTTAAAGGCCCGATGATAATGAAGGGTTATTAT
AATAATGAAGAAGCTACTAAAGCAATTATTGATAATGACGGATGGTTGCGCT
CTGGTGATATTGCTTATTATGACAATGATGGCCATTTTATATTGTGGACAGG
CTGAAGTCACTGATTAAATATAAAGGTTATCAGGTTGCACCTGCTGAAATTG
AGGGAATACTCTTACAACATCCGTATATTGTTGATGCCGGCGTTACTGGTATA
35 CCGGATGAAGCCGCGGGCGAGCTTCCAGCTGCAGGTGTTGTAGTACAGACTG
GAAAATATCTAAACGAACAAATCGTACAAGATTATGTTGCCAGTCAAGTTTC
AACAGCCAAATGGCTACGTGGTGGGGTGATATTTTGGATGAAATTCCCAA
GGATCAACTGGAAAAATTGACAGAAAAGTGTTAAGACAAATGTTAGAAAAA
CACACCAATGGG

146-1H2 (SEQ ID NO:8)

GGATCCAATGGCAGATAAGAATATTTTATATGGGCCCCGAACCATTTTATCCCT
TGGAAGATGGGACGGCTGGAGAACAGATGTTTGACGCATTATCTCGTTATGC
AGCTATTCCGGGCTGCATAGCATTGACAAATGCTCATACAAAAGAAAATGTT
45 TTATATGAAGAGTTTCTGAAACTGTCGTGTCGTTTAGCGGAAAGTTTTAAAAA
GTATGGATTA AAAACAAAACGACACAATAGCGGTGTGTAGCGAAAATAGTCTG
CAATTTTTCCTTCCTGTAATTGCATCATTGTATCTTGGAATAATTGTGGCACCT

5 GTTAACGATAAATACATTGAACGTGAATTAATACACAGTCTTGGTATTGTAA
AACCACGCATAGTTTTTTGCTCCAAGAATACTTTTCAAAAAGTACTGAATGTA
AAATCTAAATTAAAATCTATTGAAACTATTATTATATTAGACTTAAATGAAGA
CTTAGGAGGTTATCAATGCCTCAACAACCTTTATTTCTCAAAATTCCGATAGTA
10 ATCTGGACGTAAAAAAATTTAAACCCTATTCTTTTAATCGAGACGATCAGGTT
GCGTCGATTATGTTTTCTTCTGGTACAACCTGGTCTGCCGAAGGGAGTCATGCT
AACTCACAAGAATATTGTTGTCACGATTTTCTATTGCAAAAGATCCTACTTTTG
GTAACGCAATTAATCCACGTCAGCAATTTTAACGGTAATACCTTTCCACCAT
GGTTTTGGTATGATGACCACATTAGGATACTTTACTTGTGGATTCCGAGTTgTT
15 CTAATGCACACGTTTGAAGAAAACTATTTCTACAATCATTACAAGATTATAA
AGTGGAAGTACTTTACTTGTACCAACATTAATGGCATTCTTGTCAAAAAGTG
CATTAGTTGAAAAGTACGATTTATCGCACTTAAAAGAAATTGCATCTGGTGG
CGCACCTTTATCAAAAGAAATTGGGGAGATGGTGAAAAAACGGTTTAAATTA
AACTTTGTCAGGCAAGGGTATGGATTAACAGAAACCACTTCGGCTGTTTTAAT
20 TACACCGAAAGGTGACGCCAAACCGGGATCAACTGGTAAAATAGTACCATTA
CACGCTGTTAAAGTTGTCGATCCTACAACAGGAAAAATTTTGGGGCCAAATG
AACCTGGAGAATTGTATTTTAAAGGCCCGATGATAATGAAGGGTTATTATAA
TAATGAAGAAGCTACTAAAGCAATTATTGATAATGACGGATGGTTGCGCTCT
25 GGTGATATTGCTTATTATGACAATGATGGCCATTTTATATTGTGGACAGGCT
GAAGTCACTGATTAAATATAAAGGTTATCAGGTTGCACCTGCTGAAATTGAG
GGAATACTCTTACAACATCCGTATATTGTTGATGCCGGCGTTACTGGTATACC
GGATGAAGCCGCGGGCGAGCTTCCAGCTGCAGGTGTTGTAGTACAGACTGGA
AAATATCTAAACGAACAAATCGTACAAGATTATGTTGCCAGTCAAGTTTCAA
CAGCCAAATGGCTACGTGGTGGGGTGAAATTTTGGATGAAATTCCCAAAGG
ATCAACTGGAAAAATTGACAGAAAAGTGTTAAGACAAATGTTAGAAAAACA
CACCAATGGG